







chain 2, page 31-34, type English

The insertion relative to gene human polyphosphatase encoding protein that share sequence similarity with animal proteins having thymospondin repeats. MMs are confined to human (11), cow (1), pig (1), dog (1), horse (1), rabbit (1), adrenal gland, uterus, foetal kidney, foetal lung and bone trapped human cells. MMs are thymospondin repeats for treating biological disorders involving endocrine cancer and development and also in thymospondin-related diseases. MMs are used as a diagnostic probe for screening libraries, assessing gene expression patterns and also in gene therapy. Intracellular matrix proteins and proteases. The present sequence is novel human protein (MM).

Sequence 1691 AA:

Query Match 100.0% Score 9346; DB 22; Length 1691;

Best local Similarity 100.0% Ident No 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1691; Conservative 0; Identical 0; Identical 0; Identical 0;

1 MSMTSPMVLIGVMSMSPFPIIAKSPAYELPEALSPGSHLEITIGEPILYKY 60

1 MSMTSPMVLIGVMSMSPFPIIAKSPAYELPEALSPGSHLEITIGEPILYKY 60

61 DDCSTNYSSTVYVGMFAWMSSTPSTGSCAAYSLKQIISGCTGDMHYKSTN 120

61 DDCSTNYSSTVYVGMFAWMSSTPSTGSCAAYSLKQIISGCTGDMHYKSTN 120

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781 NNVVPPPIIINQSTLNIENIENIENIENIENIENIENIENIENIENIENIENI 840

781 NNVVPPPIIINQSTLNIENIENIENIENIENIENIENIENIENIENIENIENI 840

841 PERVGGVAVGPEPILSEPPPELITLVVSGGVEVSTVIRSEITLITLVV 900

841 PERVGGVAVGPEPILSEPPPELITLVVSGGVEVSTVIRSEITLITLVV 900

842 RYKQY 900

842 RYKQY 900

843 VGVVGGVAVGPEPILSEPPPELITLVVSGGVEVSTVIRSEITLITLVV 960

843 VGVVGGVAVGPEPILSEPPPELITLVVSGGVEVSTVIRSEITLITLVV 960

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861 VGVVGGVAVGPEPILSEPPPELITLVVSGGVEVSTVIRSEITLITLVV 960

861 VGVVGGVAVGPEPILSEPPPELITLVVSGGVEVSTVIRSEITLITLVV 960

862 VGVVGGVAVGPEPILSEPPPELITLVVSGGVEVSTVIRSEITLITLVV 960

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53	Sequence	874 AA:
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Search completed: August 18, 2002, 07:44:24
Job 1201: 2215 sec.

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0Y	2491	-----	2490
1b	3059	agaaataactgtctgttaagacttgaagaaatctatagagcagaataagatacaagaat	4118
0Y	2491	-----	2490
1b	3119	gaatcaaaaacagaaatccagataagcatagatccgttaaaaaaggtcagagatgaa	4178
0Y	2491	-----	2490
1b	3179	ataatccatctgtctaggttaagcctaaatgaactaacaattatataagaacataac	4238
0Y	2491	-----	2490
1b	3239	ataaatatccagaaatctagcatatctaaataataatgaaatctaatctgaatttgc	4298
0Y	2491	-----	2490
1b	3299	agagatgattatgaatgataaggttgcagctgtatcccaacacattcatctgaattgc	4358
0Y	2491	-----	2490
1b	3359	aattcccatattccatgattctgagagagaaactgaattgaatataatgaatcattgc	4418
0Y	2491	-----	2490
1b	3419	ggcagattcccatcattctctgagtgatataatgaatctccatgagatcttaatgatt	4478
0Y	2491	-----	2490
1b	3479	tataagagattcccatcttctgcttgagctctcatctctcttgcctgctatctatagac	4538
0Y	2491	-----	2490
1b	3539	gtctatcttccctcttgccttctgctgcacataattaaatctcccatagcaactgaa	4598
0Y	2491	-----	2490
1b	3599	ctgaattctatgaatctctctccctataaattaaatctctggaatgctcttataa	4658
0Y	2491	-----	2490
1b	3659	caacataagattgaactaatacagtagagaaatgtaattgctctatttcccatccct	4718
0Y	2491	-----	2490
1b	3719	cttagtaacgaatgaataaactactctctgaatccaatgtccattgaataactatcca	4778
0Y	2491	-----	2490
1b	3779	aactctctgattgatttatttaactctcttatttaacttaaaatgctcttccagaattat	4838
0Y	2491	-----	2490
1b	3839	atcaatgatttaaaaatatcaaacattcaaacacttaatttttaacttaattctcttctt	4898
0Y	2491	-----	2490
1b	3899	lctaatatctctaatlaaataattgcattaaatttttaagttgaaaaaataaaaaaada	3958
0Y	2491	-tgttctgtccagtgtgtgatttgaatccagaaaaaaacagcaggttatatcaaacctgac	2599
1b	3959	atgttctgtctaatcttgcagtggttggaatccagaaaaaaacagcaggttatatcaaacctgac	4018
0Y	2556	aaatcaaatctgcagatctacacccctcagctgaagatgattctacacagactacacagatttc	2609
1b	4019	agcccaaaagctccagatctacacccctcagctgaagatgattctacacagacttc	4078
0Y	2610	tctcttgaagatttttgcagattgctgaattgcttttaaatccaaatccagaaatgaatataa	2699
1b	4079	tctcttgaagatttttgcagattgctgaattgctttttaaataccaaatccagaaatgaatataa	4148

The insertion relates to the human protein-kinase encoding protein that share sequence similarity with animal proteins having thrombospondin repeats. Ntpe are expressed in human cell lines, pituitary, lymph nodes, prostate, testis, adrenal gland, uterus, foetal kidney, foetal lung and bone trapped human cells. Ntpe are thrombospondin useful for treating biological disorders involving angiogenesis, cancer and development and also in pharmacogenetic applications. Ntpe are useful as a hybridisation probe for screening libraries, assessing gene expression patterns and also in gene therapy. Protein kinase thrombospondin repeats act as receptors, secreted extracellular matrix proteins and proteases. The present sequence is a cDNA encoding novel human protein (Ntpe).

Sequence 2416 bp: 617 A: 675 C: 616 G: 508 T: 0 other:

Query: March 42.9% Score: 2180 DB: 22 Length: 2216
Best local similarity: 100.0% Id: 100.0%
Matches: 2180 Conservative 0 Mismatches 0 Gaps 0

QY 311 ctgaaggaatttgaagaggaagacattcgtatcaagaatgcagcatatgacg 370
DB ctgaaggaatttgaagaggaagacattcgtatcaagaatgcagcatatgacg 148
QY 371 ctgaaggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 430
DB ctgaaggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 208
QY 431 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 490
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 268
QY 491 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 550
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 328
QY 551 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 610
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 388
QY 611 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 670
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QY 671 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 730
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QY 731 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 790
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 568
QY 791 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 850
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 628
QY 851 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 910
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QY 911 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 970
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QY 971 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1030
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 808
QY 1031 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1090
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 868
QY 1091 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1150

DB 856 ctgaaggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 928
QY 1151 ctgaaggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1210
DB ctgaaggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 988
QY 1211 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1270
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1048
QY 1271 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1330
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QY 1331 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1390
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QY 1391 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1450
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QY 1511 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1570
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QY 1571 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1630
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QY 1691 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1750
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QY 1811 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1870
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1648
QY 1871 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1930
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1708
QY 1931 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1990
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1768
QY 1991 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 2050
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1828
QY 2051 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 2110
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1888
QY 2111 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 2170
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 1948
QY 2171 aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 2230
DB aggggaatttgaagaggaagacattcgtatcaagaatgcagcatatg 2008

16	AAAGAAACAGCGTATTTCGAAAGACCTGGACGAGCTGCAATGACAGCGTGGAGCGG	1528
17	TTCTGATTCGCGGAGGATGAGATGCGCGTGTGTCTCTGAGATTTACGAGAGTTAGAGTTG	1810
18	TGTAGATGCGCAAGATTAAGATGGAGCTGGTGTCTGTATGATGACGAGATGAGATGAGC	1588
19	TGCGGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAGAGAG	1670
20	TGCGGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAGAGAG	1648
21	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	1768
22	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	1900
23	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	1708
24	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	2050
25	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	1828
26	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	2110
27	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	1888
28	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	2170
29	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	1948
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31	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	2008
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49	CGTATTTAGAGAGAGAGATTTAGAGATGCGTAAAGATGAGAGAGAGAGAGAGAGAG	2548
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[illegible][illegible]

Only 1 participant

47.16, 2001-2499, 1456, length 2538

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07	1751	taagagctgcagagatgaatgaatgaatgttctctctctctctctctctctctctctctctct	1810
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07	1811	taacagagagagatgttgaagagccgcagatcacacacagagagagagagagagagagagag	1870
Db	1589	TGCGGAGGAGAGAGTGTGAAGAGGAGGAGAGTGGCCAGCAAGAGAGAGAGAGAGAGAG	1648
07	1871	catctgagtgag	1930
Db	1649	CATGTGATTAATATTCGGGCTTGGGAGATTAAGCAATCTTCTCTAGCACTAGTAA	1708
07	1941	cgaatctcagatcagagatagcctgaatctaacacccagagagagagagagagagagagag	1990
Db	1709	CGACTTACGATTCGATATACAGCTGGCTTACAGCCCTTGCAAGCAATGCTTGGAGAGTG	1768
07	1991	atccag	2050
Db	1769	ATCAAGAGAGATAGAGATGTGGTTATATATAGAGAGAGAGAGAGAGAGAGAGAT	1828
07	2051	tatctgagatagatcagagctgcagagctgaagcagagagctgaagcagagagagagag	2110
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07	2111	cggcag	2170
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07	2171	ag	2230
Db	1949	AGAGCCAGAGATGTATTTGCTTGAATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGT	2008
07	2231	tgatgag	2290
Db	2009	GAGATGAAG	2068
07	2291	ag	2350
Db	2069	ACATTGAGAGATAG	2128
07	2351	taag	2410
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07	2471	cctgag	2530
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the 1990s, the number of people in the world who are under 15 years of age has increased from 1.1 billion to 1.5 billion, and the number of people aged 65 and over has increased from 0.2 billion to 0.5 billion (United Nations 1999).

There is a growing awareness of the need to address the needs of the young and the old in the context of the ageing of the population. The United Nations (1999) has identified the need to address the needs of the young and the old as a key challenge for the 21st century.

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Result No. 1
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Matches: 1022; Consistent: 0; Mismatch: 1;
Inlets: 0; Cape: 0

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E2 00MAIN 659 615 1ST TIME 1
E3 00MAIN 616 624 6YS RICH
E4 00MAIN 725 857 SPACER
E5 00MAIN 858 907 1ST TYPE 1 2
E6 00MAIN 908 967 1ST TIME 1 2
E7 00MAIN 194 196 POLY ARG
E8 00MAIN 547 547 N-LINKED (GICAC) (POLYMER)
E9 00MAIN 724 724 N-LINKED (GICAC) (POLYMER)
E10 00MAIN 762 762 N-LINKED (GICAC) (POLYMER)
E11 00MAIN 945 945 N-LINKED (GICAC) (POLYMER)
E12 00MAIN 21 21 V (IN PER) 2
E13 00MAIN 26 41 KTSQSG V (IN PER) 2
E14 00MAIN 49 49 V - A (IN PER) 2
E15 00MAIN 72 72 V - P (IN PER) 2
E16 00MAIN 79 79 V - P (IN PER) 2
E17 00MAIN 219 219 F - G (IN PER) 2
E18 00MAIN 249 249 F - G (IN PER) 2
E19 00MAIN 265 265 MLV - S (IN PER) 2
E20 00MAIN 607 607 S - S (IN PER) 2
E21 00MAIN 936 936 L - S (IN PER) 2
E22 00MAIN 962 962 L - S (IN PER) 2
E23 00MAIN 967 967 1ST TIME 1
E24 00MAIN 105705 105705 1ST TIME 1

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Query Match 6 18: Score 584 51 18 1: Length 467
Rec'd Local Similarity 25.7% Rec'd No. 26 29
Matches 132: Conserved 75: Mismatches 176: Indels 94: Gaps 16:

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E1 00MAIN 476 558 DISTINCTION LINE
E2 00MAIN 659 615 1ST TIME 1
E3 00MAIN 616 624 6YS RICH
E4 00MAIN 725 857 SPACER
E5 00MAIN 858 907 1ST TYPE 1 2
E6 00MAIN 908 967 1ST TIME 1 2
E7 00MAIN 194 196 POLY ARG
E8 00MAIN 547 547 N-LINKED (GICAC) (POLYMER)
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E17 00MAIN 219 219 F - G (IN PER) 2
E18 00MAIN 249 249 F - G (IN PER) 2
E19 00MAIN 265 265 MLV - S (IN PER) 2
E20 00MAIN 607 607 S - S (IN PER) 2
E21 00MAIN 936 936 L - S (IN PER) 2
E22 00MAIN 962 962 L - S (IN PER) 2
E23 00MAIN 967 967 1ST TIME 1
E24 00MAIN 105705 105705 1ST TIME 1

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E1 00MAIN 476 558 DISTINCTION LINE
E2 00MAIN 659 615 1ST TIME 1
E3 00MAIN 616 624 6YS RICH
E4 00MAIN 725 857 SPACER
E5 00MAIN 858 907 1ST TYPE 1 2
E6 00MAIN 908 967 1ST TIME 1 2
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UNITED STATES OF AMERICA

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COGNATE.
From NUT, *Acacia*, and *nut*, *A. acuta* (L.) DC. (2000).
MUTUALINE.
From *mut*, *Acacia*, and *line*, *A. lineata* (L.) DC. (2000).
MUTUALINE.
From *mut*, *Acacia*, and *line*, *A. lineata* (L.) DC. (2000).

The ability of various methods to predict the effect of a mutation on protein function is an important problem in genomics. Although a number of methods have been proposed for this task, no method has been shown to be able to predict the effect of a mutation on protein function with high accuracy. In this paper, we present a new method for predicting the effect of a mutation on protein function, called *Protein Function Prediction (PFP)*. This method is based on the idea that the effect of a mutation on protein function can be predicted by analyzing the change in the protein's structure and function. We show that PFP is able to predict the effect of a mutation on protein function with high accuracy, and that it is able to predict the effect of a mutation on protein function with high accuracy.

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